Fig. 4A

SEQ ID No. 3. Nucleotide sequence of *slpA* from *Clostridium difficile* strain 171500, PCR type 1, with translation. The putative secretory signal cleavage site (Δ) and site of cleavage to form the two mature SLPs (♦) are indicated.

```
  1  ATGAATAAGAAAAATATAGCAATAGCTATGTCAGGTTTAACAGTTTTAGCTTCGGCTGCA   60
     ---------+---------+---------+---------+---------+---------+
  1  M  N  K  K  N  I  A  I  A  M  S  G  L  T  V  L  A  S  A  A   20

 61  CCTGTATTTGCAGATGATACAAAAGTTGAAACTGGTGATCAAGGATATACAGTGGTACAA  120
     ---------+---------+---------+---------+---------+---------+
 21  P  V  F  A  D  D  T  K  V  E  T  G  D  Q  G  Y  T  V  V  Q   40
              Δ

121  AGCAAGTATAAGAAAGCTGTTGAACAATTACAAAAAGGAATATTAGATGGAAGTATAACA  180
     ---------+---------+---------+---------+---------+---------+
 41  S  K  Y  K  K  A  V  E  Q  L  Q  K  G  I  L  D  G  S  I  T   60

181  GAAATTAAAGTTTTCTTTGAGGGAACTTTAGCATCTACTATAAAAGTAGGTTCTGAGCTT  240
     ---------+---------+---------+---------+---------+---------+
 61  E  I  K  V  F  F  E  G  T  L  A  S  T  I  K  V  G  S  E  L   80

241  AATGCAGCAGATGCAAGTAAATTATTGTTTACACAAGTAGATAATAAACTAGATAATTTA  300
     ---------+---------+---------+---------+---------+---------+
 81  N  A  A  D  A  S  K  L  L  F  T  Q  V  D  N  K  L  D  N  L  100

301  GGTGATGGAGATTATGTAGATTTCTTAATAACTTCTCCAGGTCAAGGGGATAAAATAACT  360
     ---------+---------+---------+---------+---------+---------+
101  G  D  G  D  Y  V  D  F  L  I  T  S  P  G  Q  G  D  K  I  T  120

361  ACAAGTAAACTTGTTGCATTGAAAGATTTAACAGGTGCTTCAGCAGATGCTATAATTGCT  420
     ---------+---------+---------+---------+---------+---------+
121  T  S  K  L  V  A  L  K  D  L  T  G  A  S  A  D  A  I  I  A  140

421  GGAACATCTTCAGCAGATGGTGTTGTTACAAATACTGGAGCTGCTAGTGGTTCTACTGAG  480
     ---------+---------+---------+---------+---------+---------+
141  G  T  S  S  A  D  G  V  V  T  N  T  G  A  A  S  G  S  T  E  160

481  ACAAATTCAGCAGGAACAAAAACTTGCAATGTCAGCTATTTTTGACACAGCATATACAGAT  540
     ---------+---------+---------+---------+---------+---------+
161  T  N  S  A  G  T  K  L  A  M  S  A  I  F  D  T  A  Y  T  D  180

541  TCATCTGAAACTGCGGTTAAGATTACTATAAAAGCAGATATGAATGATACTAAATTTGGT  600
     ---------+---------+---------+---------+---------+---------+
181  S  S  E  T  A  V  K  I  T  I  K  A  D  M  N  D  T  K  F  G  200

601  AAAGCAGGTGAGACAACTTATTCAACTGGGCTTACATTTGAAGATGGGTCTACAGAAAAA  660
     ---------+---------+---------+---------+---------+---------+
201  K  A  G  E  T  T  Y  S  T  G  L  T  F  E  D  G  S  T  E  K  220
```

Fig. 4B

```
 661  ATTGTTAAATTAGGGGACAGTGATATTATAGATATAACTAAAGCTCTTAAACTTACTGTT   720
      ---------+---------+---------+---------+---------+---------+
 221   I  V  K  L  G  D  S  D  I  I  D  I  T  K  A  L  K  L  T  V    240


 721  GTTCCTGGAAGTAAAGCAACTGTTAAGTTTGCTGAAAAAACACCAAGTGCCAGTGTTCAA   780
      ---------+---------+---------+---------+---------+---------+
 241   V  P  G  S  K  A  T  V  K  F  A  E  K  T  P  S  A  S  V  Q    260


 781  CCAGTAATAACAAAGCTTAGAATAATAAATGCTAAAGAAGAAACAATAGATATTGACGCT   840
      ---------+---------+---------+---------+---------+---------+
 261   P  V  I  T  K  L  R  I  I  N  A  K  E  E  T  I  D  I  D  A    280


 841  AGTTCTAGTAAAACAGCACAAGATTTAGCTAAAAAATATGTATTTAATAAAACTGATTTA   900
      ---------+---------+---------+---------+---------+---------+
 281   S  S  S  K  T  A  Q  D  L  A  K  K  Y  V  F  N  K  T  D  L    300


 901  AATACTCTTTATAAAGTATTAAATGGAGATGAAGCAGATACTAATGGATTAATAGAAGAA   960
      ---------+---------+---------+---------+---------+---------+
 301   N  T  L  Y  K  V  L  N  G  D  E  A  D  T  N  G  L  I  E  E    320


 961  GTTAGTGGAAAAATATCAAGTAGTTCTTTATCCAGAAGGAAAAAGAGTTACAACTAAGAGT  1020
      ---------+---------+---------+---------+---------+---------+
 321   V  S  G  K  Y  Q  V  V  L  Y  P  E  G  K  R  V  T  T  K  S    340


1021  GCTGCAAAGGCTTCAATTGCTGATGAAAATTCACCAGTTAAATTAACTCTTAAGTCAGAT  1080
      ---------+---------+---------+---------+---------+---------+
 341   A  A  K  A  S  I  A  D  E  N  S  P  V  K  L  T  L  K  S  D    360


1081  AAGAAGAAAGACTTAAAAGATTATGTGGATGATTTAAGAACATATAATAATGGATATTCA  1140
      ---------+---------+---------+---------+---------+---------+
 361   K  K  K  D  L  K  D  Y  V  D  D  L  R  T  Y  N  N  G  Y  S    380


1141  AATGCTATAGAAGTAGCAGGAGAAGATAGAATAGAAACTGCAATAGCATTAAGTCAAAAA  1200
      ---------+---------+---------+---------+---------+---------+
 381   N  A  I  E  V  A  G  E  D  R  I  E  T  A  I  A  L  S  Q  K    400


1201  TATTATAACTCTGATGATGAAAATGCTATATTTAGAGATTCAGTTGATAATGTAGTATTG  1260
      ---------+---------+---------+---------+---------+---------+
 401   Y  Y  N  S  D  D  E  N  A  I  F  R  D  S  V  D  N  V  V  L    420


1261  GTTGGAGGAAATGCAATAGTTGATGGACTTGTAGCTTCTCCTTTAGCTTCTGAAAAGAAA  1320
      ---------+---------+---------+---------+---------+---------+
 421   V  G  G  N  A  I  V  D  G  L  V  A  S  P  L  A  S  E  K  K    440


1321  GCTCCTTTATTATTAACTTCAAAAGATAAATTAGATTCAAGCGTAAAAGCTGAAATAAAG  1380
      ---------+---------+---------+---------+---------+---------+
 441   A  P  L  L  L  T  S  K  D  K  L  D  S  S  V  K  A  E  I  K    460
```

Fig. 4C

```
1381  AGAGTTATGAATATAAAGAGTACAACAGGTATAAATACTTCAAAGAAAGTTTATTTAGCT  1440
      ---------+---------+---------+---------+---------+---------+
 461  R  V  M  N  I  K  S  T  T  G  I  N  T  S  K  K  V  Y  L  A   480


1441  GGTGGAGTTAATTCTATATCTAAAGAAGTAGAAAATGAATTAAAAGATATGGGACTTAAA  1500
      ---------+---------+---------+---------+---------+---------+
 481  G  G  V  N  S  I  S  K  E  V  E  N  E  L  K  D  M  G  L  K   500


1501  GTTACAAGATTAGCAGGAGATGATAGATATGAAACTTCTCTAAAAATAGCTGATGAAGTA  1560
      ---------+---------+---------+---------+---------+---------+
 501  V  T  R  L  A  G  D  D  R  Y  E  T  S  L  K  I  A  D  E  V   520


1561  GGTCTTGATAATGATAAAGCATTTGTAGTTGGAGGAACAGGATTAGCAGATGCCATGAGT  1620
      ---------+---------+---------+---------+---------+---------+
 521  G  L  D  N  D  K  A  F  V  V  G  G  T  G  L  A  D  A  M  S   540


1621  ATAGCTCCAGTTGCATCTCAATTAAGAAATGCTAATGGTAAAATGGATTTAGCTGATGGT  1680
      ---------+---------+---------+---------+---------+---------+
 541  I  A  P  V  A  S  Q  L  R  N  A  N  G  K  M  D  L  A  D  G   560


1681  GATGCTACACCAATAGTAGTTGTAGATGGAAAAGCTAAAACTATAAATGATGATGTAAAA  1740
      ---------+---------+---------+---------+---------+---------+
 561  D  A  T  P  I  V  V  V  D  G  K  A  K  T  I  N  D  D  V  K   580


1741  GATTTCTTAGATGATTCACAAGTTGATATAATAGGTGGAGAAAACAGTGTATCTAAAGAT  1800
      ---------+---------+---------+---------+---------+---------+
 581  D  F  L  D  D  S  Q  V  D  I  I  G  G  E  N  S  V  S  K  D   600


1801  GTTGAAAATGCAATAGATGATGCTACAGGTAAATCTCCAGATAGATATAGTGGAGATGAT  1860
      ---------+---------+---------+---------+---------+---------+
 601  V  E  N  A  I  D  D  A  T  G  K  S  P  D  R  Y  S  G  D  D   620


1861  AGACAAGCAACTAATGCAAAAGTTATAAAAGAATCTTCTTATTATCAAGATAACTTAAAT  1920
      ---------+---------+---------+---------+---------+---------+
 621  R  Q  A  T  N  A  K  V  I  K  E  S  S  Y  Y  Q  D  N  L  N   640


1921  AATGATAAAAAAGTAGTTAATTTCTTTGTAGCTAAAGATGGTTCTACTAAAGAAGATCAA  1980
      ---------+---------+---------+---------+---------+---------+
 641  N  D  K  K  V  V  N  F  F  V  A  K  D  G  S  T  K  E  D  Q   660


1981  TTAGTTGATGCTTTAGCAGCAGCTCCAGTTGCAGCAAACTTTGGTGTAACTCTTAATTCT  2040
      ---------+---------+---------+---------+---------+---------+
 661  L  V  D  A  L  A  A  A  P  V  A  A  N  F  G  V  T  L  N  S   680


2041  GATGGTAAGCCAGTAGATAAAGATGGTAAAGtATTAACTGGTTCTGATAATGATAAAAAT  2100
      ---------+---------+---------+---------+---------+---------+
 681  D  G  K  P  V  D  K  D  G  K  V  L  T  G  S  D  N  D  K  N   700


2101  AAATTAGTATCTCCAGCACCTATAGTATTAGCTACTGATTCTTTATCTTCAGATCaAAGT  2160
      ---------+---------+---------+---------+---------+---------+
 701  K  L  V  S  P  A  P  I  V  L  A  T  D  S  L  S  S  D  Q  S   720
```

Fig. 4D

```
2161   GTATCTATAAGTAaAGTTCTTGATAAAGATAATGGAGAAAACTTAGTTCAAGTTGGTAAA   -2220
       ---------+---------+---------+---------+---------+---------+
 721   V   S   I   S   K   V   L   D   K   D   N   G   E   N   L   V   Q   V   G   K       740


2221   GGTATAGCTACTTCAGTTATAAACAAAATGAAAGATTTATTAGATATG  2268
       ---------+---------+---------+---------+--------
 741   G   I   A   T   S   V   I   N   K   M   K   D   L   L   D   M       756
```

Fig. 5A

SEQ ID No. 4. Nucleotide sequence of *slpA* from *Clostridium difficile* strain 172450, PCR type 5, with translation. The putative secretory signal cleavage site (Δ) is indicated, and an approximation of the and site of cleavage to form the two mature SLPs (♦) is also indicated.

```
  1  ATGAAAAAAAGAAATTTAGCAATGGCTATGGCAGCTGTTACTGTAGTAGGTTCTGCTGCT   60
     ---------+---------+---------+---------+---------+---------+
  1   M  K  K  R  N  L  A  M  A  M  A  A  V  T  V  V  G  S  A  A   20

 61  CCAGTTTTTGCAGCAGCTTCAGATGTAATATCACTACAAGATGGTACAAATGATAAGTAT  120
     ---------+---------+---------+---------+---------+---------+
 21   P  V  F  A  A  A  S  D  V  I  S  L  Q  D  G  T  N  D  K  Y   40
                  Δ

121  ACAGTATCAAATACTAAAGCTAGTGACTTAGTAAAGGATATTTTAGCAGCACAAAACTTA  180
     ---------+---------+---------+---------+---------+---------+
 41   T  V  S  N  T  K  A  S  D  L  V  K  D  I  L  A  A  Q  N  L   60

181  ACAACAGGTGCAGTTATTTTGAACAAAGATACAAAAGTTACTTTCTATGATGCAAATGAG  240
     ---------+---------+---------+---------+---------+---------+
 61   T  T  G  A  V  I  L  N  K  D  T  K  V  T  F  Y  D  A  N  E   80

241  AAAGATTCTTCAACTCCAACTGGAGATAAAAAAGTTTATTCAGAACAAACTTTAACTACA  300
     ---------+---------+---------+---------+---------+---------+
 81   K  D  S  S  T  P  T  G  D  K  K  V  Y  S  E  Q  T  L  T  T  100

301  GCTAATGGAAATGAAGATTATGTAAAGACAACTTTAAAAAAATTTAGATGCAGGAGAATAT  360
     ---------+---------+---------+---------+---------+---------+
101   A  N  G  N  E  D  Y  V  K  T  T  L  K  N  L  D  A  G  E  Y  120

361  GCTATTATAGATTTAACTTATAATAATGCTAAAACTGTTGAAATTAAAGTAGTAGCAGCT  420
     ---------+---------+---------+---------+---------+---------+
121   A  I  I  D  L  T  Y  N  N  A  K  T  V  E  I  K  V  V  A  A  140

421  AGTGAAAAAACAGTAGTTGTATCTAGTGATGCGAAAAATAGTGCAAAAGATATAGCTGAA  480
     ---------+---------+---------+---------+---------+---------+
141   S  E  K  T  V  V  V  S  S  D  A  K  N  S  A  K  D  I  A  E  160

481  AAATATGTGTTTGAAGACAAAGACTTAGAAAATGCACTAAAAACTATAAATGCCTCAGAT  540
     ---------+---------+---------+---------+---------+---------+
161   K  Y  V  F  E  D  K  D  L  E  N  A  L  K  T  I  N  A  S  D  180

541  TTCAGTAAAACTGATAGTTACTATCAAGTAGTTCTTTATCCAAAAGGAAAGAGATTACAA  600
     ---------+---------+---------+---------+---------+---------+
181   F  S  K  T  D  S  Y  Y  Q  V  V  L  Y  P  K  G  K  R  L  Q  200

601  GGTTTCTCAACTTATAGAGCTACAAATTATAATGAAGGAACTGCATATGGTAATACACCA  660
     ---------+---------+---------+---------+---------+---------+
201   G  F  S  T  Y  R  A  T  N  Y  N  E  G  T  A  Y  G  N  T  P  220
                         ♦
```

Fig. 5B

```
661   GTAATATTAACTCTAAAATCTACTAGTAAGAGTAATTTAAAGACTGCAGTAGAAGAGTTA    720
      ---------+---------+---------+---------+---------+---------+
221    V  I  L  T  L  K  S  T  S  K  S  N  L  K  T  A  V  E  E  L    240


721   CAAAAATTGAATGCTAGTTATTCTAATACTACAACTTTAGCTGGTGATGACAGAATACAA    780
      ---------+---------+---------+---------+---------+---------+
241    Q  K  L  N  A  S  Y  S  N  T  T  T  L  A  G  D  D  R  I  Q    260


781   ACAGCTATAGAGATAAGTAAAGAATATTACAATAATGATGGCGAGAAATCAGATCATTCA    840
      ---------+---------+---------+---------+---------+---------+
261    T  A  I  E  I  S  K  E  Y  Y  N  N  D  G  E  K  S  D  H  S    280


841   GCTGATGTTAAAGAGAATGTTAAAAATGTTGTATTAGTAGGTGCAAATGCACTAGTAGAT    900
      ---------+---------+---------+---------+---------+---------+
281    A  D  V  K  E  N  V  K  N  V  V  L  V  G  A  N  A  L  V  D   .300


901   GGATTAGTTGCGGCTCCTTTAGCAGCAGAAAAAGATGCTCCACTATTATTAACTTCAAAA    960
      ---------+---------+---------+---------+---------+---------+
301    G  L  V  A  A  P  L  A  A  E  K  D  A  P  L  L  L  T  S  K    320


961   GATAAATTAGATTCGTCAGTAAAATCTGAAATAAAGAGAGTTTTAGACTTAAAAACTTCA   1020
      ---------+---------+---------+---------+---------+---------+
321    D  K  L  D  S  S  V  K  S  E  I  K  R  V  L  D  L  K  T  S    340


1021  ACAGAAGTAACAGGAAAAACAGTTTATATAGCTGGTGGAGTTAATAGTGTATCTAAAGAA   1080
      ---------+---------+---------+---------+---------+---------+
341    T  E  V  T  G  K  T  V  Y  I  A  G  G  V  N  S .V  S  K  E    360


1081  GTTGTAACAGAATTAGAATCAATGGGATTAAAAGTTGAAAGATTCTCAGGTGATGATAGA   1140
      ---------+---------+---------+---------+---------+---------+
361    V  V  T  E  L  E  S  M  G  L  K  V  E  R  F  S  G  D  D  R    380


1141  TATGAAACTTCTTTAAAAAATAGCAGGTGAAATAGGCTTAGATAATGATAAGGCTTATGTA   1200
      ---------+---------+---------+---------+---------+---------+
381    Y  E  T  S  L  K  I  A  G  E  I  G  L  D  N  D  K  A  Y  V    400


1201  GTTGGTGGAACAGGATTAGCAGATGCCATGAGTATAGCTTCAGTTGCTTCTACTAAATTA   1260
      ---------+---------+---------+---------+---------+---------+
401    V  G  G  T  G  L  A  D  A  M  S  I  A  S  V  A  S  T  K  L    420


1261  GATGGTAATGGTGTTGTAGATAGAACAAATGGACATGCTACTCCAATAGTTGTTGTAGAT   1320
      ---------+---------+---------+---------+---------+---------+
421    D  G  N  G  V  V  D  R  T  N  G  H  A  T  P  I  V  V  V  D    440

1321  GGAAAAGCTGATAAAATATCTGATGACTTAGATAGTTTCTTAGGAAGCGCTGATGTAGAT   1380
      ---------+---------+---------+---------+---------+---------+
441    G  K  A  D  K  I  S  D  D  L  D  S  F  L  G  S  A  D  V  D    460


1381  ATAATAGGTGGATTTGCAAGTGTATCTGAAAAGATGGAAGAAGCTATATCAGATGCTACT   1440
      ---------+---------+---------+---------+---------+---------+
461    I  I  G  G  F  A  S  V  S  E  K  M  E  E  A  I  S  D  A  T    480
```

Fig. 5C

```
1441 GGTAAAGGCGTTACAAGAGTTAAAGGCGACGATAGACAAGACACTAACTCTGAAGTTATA 1500
     ---------+---------+---------+---------+---------+---------+
 481  G  K  G  V  T  R  V  K  G  D  D  R  Q  D  T  N  S  E  V  I  500


1501 AAAACATATTATGCTAATGATACTGAAATAGCTAAAGCTGCAGTTTTAGATAAAGATTCA 1560
     ---------+---------+---------+---------+---------+---------+
 501  K  T  Y  Y  A  N  D  T  E  I  A  K  A  A  V  L  D  K  D  S  520


1561 GGTGCTTCAAGTAGTGATGCAGGAGTATTTAATTTCTATGTAGCTAAAGATGGATCTACA 1620
     ---------+---------+---------+---------+---------+---------+
 521  G  A  S  S  S  D  A  G  V  F  N  F  Y  V  A  K  D  G  S  T  540


1621 AAAGAAGATCAATTAGTTGATGCATTAGCAGTAGGAGCTGTTGCTGGATATAAACTTGCT 1680
     ---------+---------+---------+---------+---------+---------+
 541  K  E  D  Q  L  V  D  A  L  A  V  G  A  V  A  G  Y  K  L  A  560


1681 CCAGTTGTATTAGCTACTGATTCTTTATCTTCTGATCAATCGGTTGCTATAAGCAAAGTT 1740
     ---------+---------+---------+---------+---------+---------+
 561  P  V  V  L  A  T  D  S  L  S  S  D  Q  S  V  A  I  S  K  V  580


1741 GTAGGAGAAAAATATTCTAAAGATTTAACACAAGTTGGTCAAGGAATAGCTAATTCAGTT 1800
     ---------+---------+---------+---------+---------+---------+
 581  V  G  E  K  Y  S  K  D  L  T  Q  V  G  Q  G  I  A  N  S  V  600


1801 ATAAACAAAATGAAAGATTTATTAGATATG 1830
     ---------+---------+---------+
 601  I  N  K  M  K  D  L  L  D  M  610
```

Fig. 6A

SEQ ID No. 5. Nucleotide sequence of *slpA* from *Clostridium difficile* strain 170324, PCR type 12, with translation. The putative secretory signal cleavage site (Δ) and site of cleavage to form the two mature SLPs (♦) are indicated.

```
  1  ATGAATAAGAAAAATATAGCAATAGCTATGTCAGGTTTAACAGTTTTAGCTTCGGCTGCT   60
     ---------+---------+---------+---------+---------+---------+
  1  M  N  K  K  N  I  A  I  A  M  S  G  L  T  V  L  A  S  A  A    20


 61  CCTGTTTTTGCTGCAACTACTGGAACACAAGGTTATACTGTAGTTAAAAACGACTGGAAA   120
     ---------+---------+---------+---------+---------+---------+
 21  P  V  F  A  A  T  T  G  T  Q  G  Y  T  V  V  K  N  D  W  K    40
              Δ


121  AAAGCAGTAAAACAATTACAAGATGGACTAAAAGATAATAGTATAGGAAAGATAACTGTA   180
     ---------+---------+---------+---------+---------+---------+
 41  K  A  V  K  Q  L  Q  D  G  L  K  D  N  S  I  G  K  I  T  V    60


181  TCTTTTAATGATGGGGTTGTGGGTGAAGTAGCTCCTAAAAGTGCTAATAAGAAAGCGGAC   240
     ---------+---------+---------+---------+---------+---------+
 61  S  F  N  D  G  V  V  G  E  V  A  P  K  S  A  N  K  K  A  D    80


241  AGAGATGCTGCAGCTGAGAAGTTATATAATCTTGTTAACACTCAATTAGATAAATTAGGT   300
     ---------+---------+---------+---------+---------+---------+
 81  R  D  A  A  A  E  K  L  Y  N  L  V  N  T  Q  L  D  K  L  G    100


301  GATGGAGATTATGTTGATTTTTCTGTAGATTATAATTTAGAAAACAAAATAATAACTAAT   360
     ---------+---------+---------+---------+---------+---------+
101  D  G  D  Y  V  D  F  S  V  D  Y  N  L  E  N  K  I  I  T  N    120


361  CAAGCAGATGCAGAAGCAATTGTTACAAAGTTAAATTCACTTAATGAGAAAACTCTTATT   420
     ---------+---------+---------+---------+---------+---------+
121  Q  A  D  A  E  A  I  V  T  K  L  N  S  L  N  E  K  T  L  I    140


421  GATATAGCAACTAAAGATACTTTTGGAATGGTTAGTAAAACACAAGATAGTGAAGGTAAA   480
     ---------+---------+---------+---------+---------+---------+
141  D  I  A  T  K  D  T  F  G  M  V  S  K  T  Q  D  S  E  G  K    160


481  AATGTTGCTGCAACAAAGGCACTTAAAGTTAAAGATGTTGCTACATTTGGTTTGAAGTCT   540
     ---------+---------+---------+---------+---------+---------+
161  N  V  A  A  T  K  A  L  K  V  K  D  V  A  T  F  G  L  K  S    180


541  GGTGGAAGCGAAGATACTGGATATGTTGTTGAAATGAAAGCAGGAGCTGTAGAGGATAAG   600
     ---------+---------+---------+---------+---------+---------+
181  G  G  S  E  D  T  G  Y  V  V  E  M  K  A  G  A  V  E  D  K    200


601  TATGGTAAAGTTGGAGATAGTACGGCAGGTATTGCAATAAATCTTCCTAGTACTGGACTT   660
     ---------+---------+---------+---------+---------+---------+
201  Y  G  K  V  G  D  S  T  A  G  I  A  I  N  L  P  S  T  G  L    220
              ♦
```

Fig. 6B

```
661  GAATATGCAGGTAAAGGAACAACAATTGATTTTAATAAAACTTTAAAAGTTGATGTAACA    720
     ---------+---------+---------+---------+---------+---------+
221  E   Y   A   G   K   G   T   T   I   D   F   N   K   T   L   K   V   D   V   T    240


721  GGTGGTTCAACACCTAGTGCTGTAGCTGTAAGTGGTTTTGTAACTAAAGATGATACTGAT    780
     ---------+---------+---------+---------+---------+---------+
241  G   G   S   T   P   S   A   V   A   V   S   G   F   V   T   K   D   D   T   D    260


781  TTAGCAAAATCAGGTACTATAAATGTAAGAGTTATAAATGCAAAAGAAGAATCAATTGAT    840
     ---------+---------+---------+---------+---------+---------+
261  L   A   K   S   G   T   I   N   V   R   V   I   N   A   K   E   E   S   I   D    280


841  ATAGATGCAAGCTCATATACATCAGCTGAAAATTTAGCTAAAAGATATGTATTTGATCCA    900
     ---------+---------+---------+---------+---------+---------+
281  I   D   A   S   S   Y   T   S   A   E   N   L   A   K   R   Y   V   F   D   P    300


901  GATGAAATTTCTGAAGCATATAAGGCAATAGTAGCATTACAAAATGATGGTATAGAGTCT    960
     ---------+---------+---------+---------+---------+---------+
301  D   E   I   S   E   A   Y   K   A   I   V   A   L   Q   N   D   G   I   E   S    320


961  AACTTAGTTCAGTTAGTTAATGGAAAATATCAAGTGATTTTTTATCCAGAAGGTAAAAGA    1020
     ---------+---------+---------+---------+---------+---------+
321  N   L   V   Q   L   V   N   G   K   Y   Q   V   I   F   Y   P   E   G   K   R    340


1021 TTAGAAACTAAATCAGCAAATGATACAATAGCTAGTCAAGATACACCAGCTAAAGTAGTT    1080
     ---------+---------+---------+---------+---------+---------+
341  L   E   T   K   S   A   N   D   T   I   A   S   Q   D   T   P   A   K   V   V    360
                     ◆


1081 ATAAAAGCTAATAAATTAAAAGATTTAAAAGATTATGTAGATGATTTAAAAACATATAAT    1140
     ---------+---------+---------+---------+---------+---------+
361  I   K   A   N   K   L   K   D   L   K   D   Y   V   D   D   L   K   T   Y   N    380


1141 AATACTTATTCAAATGTTGTAACAGTAGCAGGAGAAGATAGAATAGAAACTGCTATAGAA    1200
     ---------+---------+---------+---------+---------+---------+
381  N   T   Y   S   N   V   V   T   V   A   G   E   D   R   I   E   T   A   I   E    400


1201 TTAAGTAGTAAATATTATAATTCTGATGATAAAAATGCAATAACTGATAAAGCAGTTAAT    1260
     ---------+---------+---------+---------+---------+---------+
401  L   S   S   K   Y   Y   N   S   D   D   K   N   A   I   T   D   K   A   V   N    420


1261 GATATAGTATTAGTTGGATCTACATCTATAGTTGATGGTCTTGTTGCATCACCATTAGCT    1320
     ---------+---------+---------+---------+---------+---------+
421  D   I   V   L   V   G   S   T   S   I   V   D   G   L   V   A   S   P   L   A    440


1321 TCAGAAAAAACAGCTCCATTATTATTAACTTCAAAAGATAAATTAGATTCATCAGTAAAA    1380
     ---------+---------+---------+---------+---------+---------+
441  S   E   K   T   A   P   L   L   L   T   S   K   D   K   L   D   S   S   V   K    460
```

Fig. 6C

```
1381 TCTGAAATAAAGAGAGTTATGAACTTAAAGAGTGACACTGGTATAAATACTTCTAAAAAA 1440
     ---------+---------+---------+---------+---------+---------+
 461  S  E  I  K  R  V  M  N  L  K  S  D  T  G  I  N  T  S  K  K   480


1441 GTTTATTTAGCTGGTGGAGTTAATTCTATATCTAAAGATGTAGAAAATGAATTGAAAAAC 1500
     ---------+---------+---------+---------+---------+---------+
 481  V  Y  L  A  G  G  V  N  S  I  S  K  D  V  E  N  E  L  K  N   500


1501 ATGGGTCTTAAAGTTACTAGATTATCAGGAGAAGACAGATACGAAACTTCTTTAGCAATA 1560
     ---------+---------+---------+---------+---------+---------+
 501  M  G  L  K  V  T  R  L  S  G  E  D  R  Y  E  T  S  L  A  I   520


1561 GCTGATGAAATAGGTCTTGATAATGATAAAGCATTTGTAGTTGGTGGTACTGGATTAGCA 1620
     ---------+---------+---------+---------+---------+---------+
 521  A  D  E  I  G  L  D  N  D  K  A  F  V  V  G  G  T  G  L  A   540


1621 GATGCTATGAGTATAGCTCCAGTTGCTTCTCAACTTAAAGATGGAGATGCTACTCCAATA 1680
     ---------+---------+---------+---------+---------+---------+
 541  D  A  M  S  I  A  P  V  A  S  Q  L  K  D  G  D  A  T  P  I   560


1681 GTAGTTGTAGATGGAAAAGCAAAAGAAATAAGTGATGATGCTAAGAGTTTCTTAGGAACT 1740
     ---------+---------+---------+---------+---------+---------+
 561  V  V  V  D  G  K  A  K  E  I  S  D  D  A  K  S  F  L  G  T   580


1741 TCTGATGTTGATATAATAGGTGGAAAAAATAGCGTATCTAAAGAGATTGAAGAGTCAATA 1800
     ---------+---------+---------+---------+---------+---------+
 581  S  D  V  D  I  I  G  G  K  N  S  V  S  K  E  I  E  E  S  I   600


1801 GATAGTGCAACTGGAAAAACTCCAGATAGAATAAGTGGAGATGATAGACAAGCAACTAAT 1860
     ---------+---------+---------+---------+---------+---------+
 601  D  S  A  T  G  K  T  P  D  R  I  S  G  D  D  R  Q  A  T  N   620


1861 GCTGAAGTTTTAAAAGAAGATGATTATTTCACAGATGGTGAAGTTGTGAATTACTTTGTT 1920
     ---------+---------+---------+---------+---------+---------+
 621  A  E  V  L  K  E  D  D  Y  F  T  D  G  E  V  V  N  Y  F  V   640


1921 GCAAAAGATGGTTCTACTAAAGAAGATCAATTAGTAGATGCCTTAGCAGCAGCACCAATA 1980
     ---------+---------+---------+---------+---------+---------+
 641  A  K  D  G  S  T  K  E  D  Q  L  V  D  A  L  A  A  A  P  I   660


1981 GCAGGTAGATTTAAGGAGTCTCCAGCTCCAATCATACTAGCTACTGATACTTTATCTTCT 2040
     ---------+---------+---------+---------+---------+---------+
 661  A  G  R  F  K  E  S  P  A  P  I  I  L  A  T  D  T  L  S  S   680


2041 GACCAAAATGTAGCTGTAAGTAAAGCAGTTCCTAAAGATGGTGGAACTAACTTAGTTCAA 2100
     ---------+---------+---------+---------+---------+---------+
 681  D  Q  N  V  A  V  S  K  A  V  P  K  D  G  G  T  N  L  V  Q   700


2101 GTAGGTAAAGGTATAGCTTCTTCAGTTATAAACAAAATGAAAGATTTATTAGATATG 2157
     ---------+---------+---------+---------+---------+-------
 701  V  G  K  G  I  A  S  S  V  I  N  K  M  K  D  L  L  D  M   719
```

Fig. 7A

SEQ ID No 6. Nucleotide sequence of *slpA* from *Clostridium difficile*
strain 171448, PCR type 12, with translation. The putative
secretory signal cleavage site (Δ) and site of cleavage to form the
two mature SLPs (♦) are indicated.

```
   1  ATGAATAAGAAAAATATAGCAATAGCTATGTCAGGTTTAACAGTTTTAGCTTCGGCTGCT   60
      ---------+---------+---------+---------+---------+---------+
   1   M  N  K  K  N  I  A  I  A  M  S  G  L  T  V  L  A  S  A  A    20


  61  CCTGTTTTTGCTGCAACTACTGGAACACAAGGTTATACTGTAGTTAAAAACGACTGGAAA   120
      ---------+---------+---------+---------+---------+---------+
  21   P  V  F  A  A  T  T  G  T  Q  G  Y  T  V  V  K  N  D  W  K    40
                  Δ

 121  AAAGCAGTAAAACAATTACAAGATGGACTAAAAGATAATAGTATAGGAAAGATAACTGTA   180
      ---------+---------+---------+---------+---------+---------+
  41   K  A  V  K  Q  L  Q  D  G  L  K  D  N  S  I  G  K  I  T  V    60


 181  TCTTTTAATGATGGGGTTGTGGGTGAAGTAGCTCCTAAAAGTGCTAATAAGAAAGCGGAC   240
      ---------+---------+---------+---------+---------+---------+
  61   S  F  N  D  G  V  V  G  E  V  A  P  K  S  A  N  K  K  A  D    80


 241  AGAGATGCTGCAGCTGAGAAGTTATATAATCTTGTTAACACTCAATTAGATAAATTAGGT   300
      ---------+---------+---------+---------+---------+---------+
  81   R  D  A  A  A  E  K  L  Y  N  L  V  N  T  Q  L  D  K  L  G    100


 301  GATGGAGATTATGTTGATTTTTCTGTAGATTATAATTTAGAAAACAAAATAATAACTAAT   360
      ---------+---------+---------+---------+---------+---------+
 101   D  G  D  Y  V  D  F  S  V  D  Y  N  L  E  N  K  I  I  T  N    120


 361  CAAGCAGATGCAGAAGCAATTGTTACAAAGTTAAATTCACTTAATGAGAAAACTCTTATT   420
      ---------+---------+---------+---------+---------+---------+
 121   Q  A  D  A  E  A  I  V  T  K  L  N  S  L  N  E  K  T  L  I    140


 421  GATATAGCAACTAAAGATACTTTTGGAATGGTTAGTAAAACACAAGATAGTGGAGGTAAA   480
      ---------+---------+---------+---------+---------+---------+
 141   D  I  A  T  K  D  T  F  G  M  V  S  K  T  Q  D  S  G  G  K    160


 481  AATGTTGCTGCAACAAAGGCACTTAAAGTTAAAGATGTTGCTACATTTGGTTTGAAGTCT   540
      ---------+---------+---------+---------+---------+---------+
 161   N  V  A  A  T  K  A  L  K  V  K  D  V  A  T  F  G  L  K  S    180


 541  GGTGGAAGCGAAGATACTGGATATGTTGTTGAAATGAAAGCAGGAGCTGTAGAGGATAAG   600
      ---------+---------+---------+---------+---------+---------+
 181   G  G  S  E  D  T  G  Y  V  V  E  M  K  A  G  A  V  E  D  K    200


 601  TATGGTAAAGTTGGAGATAGTACGGCAGGTATTGCAATAAATCTTCCTAGTACTGGACTT   660
      ---------+---------+---------+---------+---------+---------+
 201   Y  G  K  V  G  D  S  T  A  G  I  A  I  N  L  P  S  T  G  L    220
```

Fig. 7B

```
661 GAATATGCAGGTAAAGGAACAACAATTGATTTTAATAAAACTTTAAAAGTTGATGTAACA   720
    ---------+---------+---------+---------+---------+---------+
221  E  Y  A  G  K  G  T  T  I  D  F  N  K  T  L  K  V  D  V  T   240


721 GGTGGTTCAACACCTAGTGCTGTAGCTGTAAGTGGTTTTGTAACTAAAGATGATACTGAT   780
    ---------+---------+---------+---------+---------+---------+
241  G  G  S  T  P  S  A  V  A  V  S  G  F  V  T  K  D  D  T  D   260


781 TTAGCAAAATCAGGTACTATAAATGTAAGAGTTATAAATGCAAAAGAAGAATCAATTGAT   840
    ---------+---------+---------+---------+---------+---------+
261  L  A  K  S  G  T  I  N  V  R  V  I  N  A  K  E  E  S  I  D   280


841 ATAGATGCAAGCTCATATACATCAGCTGAAAATTTAGCTAAAAGATATGTATTTGATCCA   900
    ---------+---------+---------+---------+---------+---------+
281  I  D  A  S  S  Y  T  S  A  E  N  L  A  K  R  Y  V  F  D  P   300


901 GATGAAATTTCTGAAGCATATAAGGCAATAGTAGCATTACAAAATGATGGTATAGAGTCT   960
    ---------+---------+---------+---------+---------+---------+
301  D  E  I  S  E  A  Y  K  A  I  V  A  L  Q  N  D  G  I  E  S   320


961 AATTTAGTTCAGTTAGTTAATGGAAAAATATCAAGTGATTTTTTATCCAGAAGGTAAAAGA   1020
    ---------+---------+---------+---------+---------+---------+
321  N  L  V  Q  L  V  N  G  K  Y  Q  V  I  F  Y  P  E  G  K  R   340


1021 TTAGAAACTAAATCAGCAAATGATACAATAGCTAGTCAAGATACACCAGCTAAAGTAGTT   1080
     ---------+---------+---------+---------+---------+---------+
341  L  E  T  K  S  A  N  D  T  I  A  S  Q  D  T  P  A  K  V  V   360
                      ♦


1081 ATAAAAGCTAATAAATTAAAAGATTTAAAAGATTATGTAGATGATTTAAAAACATATAAT   1140
     ---------+---------+---------+---------+---------+---------+
361  I  K  A  N  K  L  K  D  L  K  D  Y  V  D  D  L  K  T  Y  N   380


1141 AATACTTATTCAAATGTTGTAACAGTAGCAGGAGAAGATAGAATAGAAACTGCTATAGAA   1200
     ---------+---------+---------+---------+---------+---------+
381  N  T  Y  S  N  V  V  T  V  A  G  E  D  R  I  E  T  A  I  E   400


1201 TTAAGTAGTAAATATTATAATTCTGATGATAAAAATGCAATAACTGATAAAGCAGTTAAT   1260
     ---------+---------+---------+---------+---------+---------+
401  L  S  S  K  Y  Y  N  S  D  D  K  N  A  I  T  D  K  A  V  N   420


1261 GATATAGTATTAGTTGGATCTACATCTATAGTTGATGGTCTTGTTGCATCACCATTAGCT   1320
     ---------+---------+---------+---------+---------+---------+
421  D  I  V  L  V  G  S  T  S  I  V  D  G  L  V  A  S  P  L  A   440


1321 TCAGAAAAAACAGCTCCATTATTATTAGCTTCAAAAGATAAATTAGATTCATCAGTAAAA   1380
     ---------+---------+---------+---------+---------+---------+
441  S  E  K  T  A  P  L  L  L  A  S  K  D  K  L  D  S  S  V  K   460


1381 TCTGAAATAAAGAGAGTTATGAACTTAAAGAGTGACACTGGTATAAATACTTCTAAAAAA   1440
     ---------+---------+---------+---------+---------+---------+
461  S  E  I  K  R  V  M  N  L  K  S  D  T  G  I  N  T  S  K  K   480
```

Fig. 7C

```
1441 GTTTATTTAGCTGGTGGAGTTAATTCTATATCTAAAGATGTAGAAAATGAATTGAAAAAC 1500
     ---------+---------+---------+---------+---------+---------+
 481  V  Y  L  A  G  G  V  N  S  I  S  K  D  V  E  N  E  L  K  N  500


1501 ATGGGTCTTAAAGTTACTAGATTATCAGGAGAAGACAGATACGAAACTTCTTTAGCAATA 1560
     ---------+---------+---------+---------+---------+---------+
 501  M  G  L  K  V  T  R  L  S  G  E  D  R  Y  E  T  S  L  A  I  520


1561 GCTGATGAAATAGGTCTTGATAATGATAAAGCATTTGTAGTTGGTGGTACTGGATTAGCA 1620
     ---------+---------+---------+---------+---------+---------+
 521  A  D  E  I  G  L  D  N  D  K  A  F  V  V  G  G  T  G  L  A  540


1621 GATGCTATGAGTATAGCTCCAGTTGCTTCTCAACTTAAAGATGGAGATGCTACTCCAATA 1680
     ---------+---------+---------+---------+---------+---------+
 541  D  A  M  S  I  A  P  V  A  S  Q  L  K  D  G  D  A  T  P  I  560


1681 GTAGTTGTAGATGGAAAAGCAAAAGAAATAAGTGATGATGCTAAGAGTTTCTTAGGAACT 1740
     ---------+---------+---------+---------+---------+---------+
 561  V  V  V  D  G  K  A  K  E  I  S  D  D  A  K  S  F  L  G  T  580


1741 TCTGATGTTGATATAATAGGTGGAAAAAAATAGCGTATCTAAAGAGATTGAAGAGTCAATA 1800
     ---------+---------+---------+---------+---------+---------+
 581  S  D  V  D  I  I  G  G  K  N  S  V  S  K  E  I  E  E  S  I  600


1801 GATAGTGCAACTGGAAAAACTCCAGATAGAATAAGTGGAGATGATAGACAAGCAACTAAT 1860
     ---------+---------+---------+---------+---------+---------+
 601  D  S  A  T  G  K  T  P  D  R  I  S  G  D  D  R  Q  A  T  N  620


1861 GCTGAAGTTTTAAAAGAAGATGATTATTTCACAGATGGTGAAGTTGTGAATTACTTTGTT 1920
     ---------+---------+---------+---------+---------+---------+
 621  A  E  V  L  K  E  D  D  Y  F  T  D  G  E  V  V  N  Y  F  V  640


1921 GCAAAAGATGGTTCTACTAAAGAAGATCAATTAGTAGATGCCTTAGCAGCAGCACCAATA 1980
     ---------+---------+---------+---------+---------+---------+
 641  A  K  D  G  S  T  K  E  D  Q  L  V  D  A  L  A  A  A  P  I  660


1981 GCAGGTAGATTTAAGGAGTCTCCAGCTCCAATCATACTAGCTACTGATACTTTATCTTCT 2040
     ---------+---------+---------+---------+---------+---------+
 661  A  G  R  F  K  E  S  P  A  P  I  I  L  A  T  D  T  L  S  S  680


2041 GACCAAAATGTAGCTGTAAGTAAAGCAGTTCCTAAAGATGGTGGAACTAACTTAGTTCAA 2100
     ---------+---------+---------+---------+---------+---------+
 681  D  Q  N  V  A  V  S  K  A  V  P  K  D  G  G  T  N  L  V  Q  700


2101 GTAGGTAAAGGTATAGCTTCTTCAGTTATAAACAAAATGAAAGATTTATTAGATATG 2157
     ---------+---------+---------+---------+---------+--------
 701  V  G  K  G  I  A  S  S  V  I  N  K  M  K  D  L  L  D  M  719
```

Fig. 8A

SEQ ID No. 7. Nucleotide sequence of slpA from Clostridium
difficile strain 171862, PCR type 17, with translation. The
putative secretory signal cleavage site (Δ) and site of cleavage to
form the two mature SLPs (♦) are indicated.

```
  1 ATGAATAAGAAAAACTTAGCAATGGCTATGGCAGCAGTTACTGTTGTGGGTTCTGCAGCG    60
    ---------+---------+---------+---------+---------+---------+
  1 M  N  K  K  N  L  A  M  A  M  A  A  V  T  V  V  G  S  A  A    20


 61 CCAATATTTGCAGATAGTACTACGCCAGGTTATACTGTAGTGAAAAATGATTGGAAAAAA   120
    ---------+---------+---------+---------+---------+---------+
 21 P  I  F  A  D  S  T  T  P  G  Y  T  V  V  K  N  D  W  K  K    40
             Δ

121 GCAGTAAAACAATTACAAGATGGGTTGAAAAATAAAACTATATCAACAATAAAGGTGTCT   180
    ---------+---------+---------+---------+---------+---------+
 41 A  V  K  Q  L  Q  D  G  L  K  N  K  T  I  S  T  I  K  V  S    60


181 TTTAATGGAAACTCTGTTGGAGAAGTTACACCAGCCAGTTCTGGAGCAAAAAAAGCAGAT   240
    ---------+---------+---------+---------+---------+---------+
 61 F  N  G  N  S  V  G  E  V  T  P  A  S  S  G  A  K  K  A  D    80


241 AGAGATGCTGCAGCTGAAAAGTTATATAATTTAGTAAATACACAATTAGATAAACTAGGT   300
    ---------+---------+---------+---------+---------+---------+
 81 R  D  A  A  A  E  K  L  Y  N  L  V  N  T  Q  L  D  K  L  G   100


301 GATGGAGATTACGTTGACTTTGAAGTAACTTATAATTTAGCTACTCAAATAATTACAAAA   360
    ---------+---------+---------+---------+---------+---------+
101 D  G  D  Y  V  D  F  E  V  T  Y  N  L  A  T  Q  I  I  T  K   120


361 GCAGAAGCAGAGGCAGTTCTTACAAAATTACAACAATATAATGATAAAGTACTTATAAAT   420
    ---------+---------+---------+---------+---------+---------+
121 A  E  A  E  A  V  L  T  K  L  Q  Q  Y  N  D  K  V  L  I  N   140


421 TCTGCAACAGATACAGTAAAAGGTATGGTATCTGATACACAAGTTGATAGCAAAAATGTT   480
    ---------+---------+---------+---------+---------+---------+
141 S  A  T  D  T  V  K  G  M  V  S  D  T  Q  V  D  S  K  N  V   160


481 GCAGCTAACCCACTTAAAGTTAGTGATATGTATACAATACCATCTGCTATTACTGGAAGT   540
    ---------+---------+---------+---------+---------+---------+
161 A  A  N  P  L  K  V  S  D  M  Y  T  I  P  S  A  I  T  G  S   180


541 GATGATTCTGGGTATAGTATTGCTAAACCAACAGAAAAGACTACAaGTTTATTGTATGGT   600
    ---------+---------+---------+---------+---------+---------+
181 D  D  S  G  Y  S  I  A  K  P  T  E  K  T  T  S  L  L  Y  G   200


601 ACGGTTGGTGATGCAACTGCAGGTAAAGCAATAACAGTAGATACAGCTTCAAATGAAGCT   660
    ---------+---------+---------+---------+---------+---------+
201 T  V  G  D  A  T  A  G  K  A  I  T  V  D  T  A  S  N  E  A   220
```

Fig. 8B

```
 661  TTTGCTGGAAATGGAAAGGTTATTGACTACAATAAATCATTCAAAGCAACTGTACAAGGA   720
      ---------+---------+---------+---------+---------+---------+
 221   F   A   G   N   G   K   V   I   D   Y   N   K   S   F   K   A   T   V   Q   G    240


 721  GATGGAACAGTTAAGACAAGCGGGGTTGTACTTAAAGATGCAAGTGATATGGCTGCAACA   780
      ---------+---------+---------+---------+---------+---------+
 241   D   G   T   V   K   T   S   G   V   V   L   K   D   A   S   D   M   A   A   T    260


 781  GGTACTATAAAAGTTAGAGTTACAAGTGCAAAAGAAGAATCTATTGATGTGGATTCAAGT   840
      ---------+---------+---------+---------+---------+---------+
 261   G   T   I   K   V   R   V   T   S   A   K   E   E   S   I   D   V   D   S   S    280


 841  TCATATATTAGTGCTGAAAATTTAGCTAAAAAATATGTATTTAATCCTAAAGAGGTTTCT   900
      ---------+---------+---------+---------+---------+---------+
 281   S   Y   I   S   A   E   N   L   A   K   K   Y   V   F   N   P   K   E   V   S    300


 901  GAAGCTTATAATGCAATAGTTGCATTACAAAATGATGGAATAGAATCTGATTTAGTACAA   960
      ---------+---------+---------+---------+---------+---------+
 301   E   A   Y   N   A   I   V   A   L   Q   N   D   G   I   E   S   D   L   V   Q    320


 961  TTAGTTAATGGAAAATATCAAGTTATTTTCTATCCAGAAGGAAAAAGATTAGAAACTAAA   1020
      ---------+---------+---------+---------+---------+---------+
 321   L   V   N   G   K   Y   Q   V   I   F   Y   P   E   G   K   R   L   E   T   K    340


1021  TCTGCAGATATAATAGCTGATGCAGATAGTCCAGCTAAAATAACTATAAAAGCTAATAAA   1080
      ---------+---------+---------+---------+---------+---------+
 341   S   A   D   I   I   A   D   A   D   S   P   A   K   I   T   I   K   A   N   K    360
        ♦

1081  TTAAAAGATTTAAAAGATTATGTAGATGATTTAAAAAACATACAATAATACTTACTCAAAT   1140
      ---------+---------+---------+---------+---------+---------+
 361   L   K   D   L   K   D   Y   V   D   D   L   K   T   Y   N   N   T   Y   S   N    380


1141  GTTGTAACAGTAGCAGGAGAAGATAGAATAGAAACTGCTATAGAATTAAGTAGTAAATAT   1200
      ---------+---------+---------+---------+---------+---------+
 381   V   V   T   V   A   G   E   D   R   I   E   T   A   I   E   L   S   S   K   Y    400


1201  TATAATTCTGATGATAAAAATGCAATAACTGATGATGCAGTTAATAATATAGTATTAGTT   1260
      ---------+---------+---------+---------+---------+---------+
 401   Y   N   S   D   D   K   N   A   I   T   D   D   A   V   N   N   I   V   L   V    420


1261  GGATCTACATCTATAGTTGATGGTCTTGTTGCATCACCATTAGCTTCAGAAAAAACAGCT   1320
      ---------+---------+---------+---------+---------+---------+
 421   G   S   T   S   I   V   D   G   L   V   A   S   P   L   A   S   E   K   T   A    440


1321  CCATTATTATTAACTTCAAAAGATAAATTAGATTCATCAGTAAAATCTGAGATAAAAAGA   1380
      ---------+---------+---------+---------+---------+---------+
 441   P   L   L   L   T   S   K   D   K   L   D   S   S   V   K   S   E   I   K   R    460


1381  GTTATGAACTTAAAGAGTGATACTGGTATAAATACTTCTAAAAAAGTTTATTTAGCTGGT   1440
      ---------+---------+---------+---------+---------+---------+
 461   V   M   N   L   K   S   D   T   G   I   N   T   S   K   K   V   Y   L   A   G    480
```

Fig. 8C

```
1441  GGAGTTAATTCTATATCTAAAGATGTAGAAGATGAATTGAAAAATATGGGCCTTAAAGTT  1500
      ---------+---------+---------+---------+---------+---------+
 481  G  V  N  S  I  S  K  D  V  E  D  E  L  K  N  M  G  L  K  V   500


1501  ACTAGATTATCAGGAGAAGACAGATACGAAACTTCTTTAGCAATAGCTGATGAAATAGGT  1560
      ---------+---------+---------+---------+---------+---------+
 501  T  R  L  S  G  E  D  R  Y  E  T  S  L  A  I  A  D  E  I  G   520


1561  CTTGATAATGATAAAGCATTTGTAGTTGGTGGTACTGGATTGGCAGATGCTATGAGTATA  1620
      ---------+---------+---------+---------+---------+---------+
 521  L  D  N  D  K  A  F  V  V  G  G  T  G  L  A  D  A  M  S  I   540


1621  GCTCCAGTTGCTTCTCAACTTAAAGATGGAGATGCTACTCCAATAGTAGTTGTAGATGGA  1680
      ---------+---------+---------+---------+---------+---------+
 541  A  P  V  A  S  Q  L  K  D  G  D  A  T  P  I  V  V  V  D  G   560


1681  AAAGCAAAAGAAATAAGTGATGATGCTAAGAGTTTCTTAGGAACTTCTGATGTTGATATA  1740
      ---------+---------+---------+---------+---------+---------+
 561  K  A  K  E  I  S  D  D  A  K  S  F  L  G  T  S  D  V  D  I   580


1741  ATAGGTGGAAAAAATAGCGTATCTAAAGAGATTGAAGAGTCAATAGATAGTGCAACTGGA  1800
      ---------+---------+---------+---------+---------+---------+
 581  I  G  G  K  N  S  V  S  K  E  I  E  E  S  I  D  S  A  T  G   600


1801  AAAACTCCAGATAGAATAAGTGGAGATGACAGACAAGCAACTAATGCTGAAGTTTTAAAA  1860
      ---------+---------+---------+---------+---------+---------+
 601  K  T  P  D  R  I  S  G  D  D  R  Q  A  T  N  A  E  V  L  K   620


1861  GAAGATGATTATTTCAAAGATGGTGAAGTTGTGAATTACTTTGTTGCAAAAGATGGTTCT  1920
      ---------+---------+---------+---------+---------+---------+
 621  E  D  D  Y  F  K  D  G  E  V  V  N  Y  F  V  A  K  D  G  S   640


1921  ACTAAAGAAGATCAATTAGTAGATGCATTAGCAGCAGCACCAATAGCAGGTAGATTTAAG  1980
      ---------+---------+---------+---------+---------+---------+
 641  T  K  E  D  Q  L  V  D  A  L  A  A  A  P  I  A  G  R  F  K   660


1981  GAGTCTCCAGCTCCAATCATACTAGCTACTGATACTTTATCTTCTGACCAAAATGTAGCT  2040
      ---------+---------+---------+---------+---------+---------+
 661  E  S  P  A  P  I  I  L  A  T  D  T  L  S  S  D  Q  N  V  A   680


2041  GTAAGTAAAGCAGTTCCTAAAGATGGTGGAACTAACTTAGTTCAAGTAGGTAAAGGTATA  2100
      ---------+---------+---------+---------+---------+---------+
 681  V  S  K  A  V  P  K  D  G  G  T  N  L  V  Q  V  G  K  G  I   700


2101  GCTTCTTCAGTTATAAACAAAATGAAAGATTTATTAGATATGTAA  2145
      ---------+---------+---------+---------+-----
 701  A  S  S  V  I  N  K  M  K  D  L  L  D  M  *   715
```

Fig. 9A

SEQ ID No 8. Nucleotide sequence of *slpA* from *Clostridium difficile*
strain 173644, PCR type 31, with translation. The putative
secretory signal cleavage site (Δ) and site of cleavage to form the
two mature SLPs (♦) are indicated.

```
  1   ATGAATAAGAAGGATATAGCAATAGCTATGTCAGGATTAACAGTATTAGCTTCTGCAGCA    60
      ---------+---------+---------+---------+---------+---------+
  1   M  N  K  K  D  I  A  I  A  M  S  G  L  T  V  L  A  S  A  A    20


 61   CCTGTATTTGCTGCTAGTAGTTTTACAGCAGATTATAATTATACTGTAGTGCAAGGAAAA   120
      ---------+---------+---------+---------+---------+---------+
 21   P  V  F  A  A  S  S  F  T  A  D  Y  N  Y  T  V  V  Q  G  K    40
                  Δ


121   TATCAAAAAGTTATAACTGGATTACAAGATGGTTTAAAAAATGGAAAAATAACAAATATT   180
      ---------+---------+---------+---------+---------+---------+
 41   Y  Q  K  V  I  T  G  L  Q  D  G  L  K  N  G  K  I  T  N  I    60


181   GATGTAATATTTGATGGAAGTTCAATTGGTGAGGTAGTGCCAGGTTCTGATGCTGCAGCT   240
      ---------+---------+---------+---------+---------+---------+
 61   D  V  I  F  D  G  S  S  I  G  E  V  V  P  G  S  D  A  A  A    80


241   GCAGCTACTAAATTAAAAAGTTTAGTTGATGATAAGTTAGATAACTTAGGTGATGGAAAA   300
      ---------+---------+---------+---------+---------+---------+
 81   A  A  T  K  L  K  S  L  V  D  D  K  L  D  N  L  G  D  G  K   100


301   TACGTTCAATTTAATGTTACTTATACTACTAAATCTATAATAACTAAAGCAGAATTAAAA   360
      ---------+---------+---------+---------+---------+---------+
101   Y  V  Q  F  N  V  T  Y  T  T  K  S  I  I  T  K  A  E  L  K   120


361   AATTATTATAATCAATTAGAAAGTAGTAAAGATAGAATACTTATAGGAAATGAACCTCAA   420
      ---------+---------+---------+---------+---------+---------+
121   N  Y  Y  N  Q  L  E  S  S  K  D  R  I  L  I  G  N  E  P  Q   140


421   GATACAGGAACTAAAGGTCTTATAAAAGCTGATACTGATGGTACTACTGCTGTTGCAGCA   480
      ---------+---------+---------+---------+---------+---------+
141   D  T  G  T  K  G  L  I  K  A  D  T  D  G  T  T  A  V  A  A   160


481   GCTGCACCATTGAAATTATCAGATATATTTACGTTTAGTTATGATGAAGTAACAGGTGTA   540
      ---------+---------+---------+---------+---------+---------+
161   A  A  P  L  K  L  S  D  I  F  T  F  S  Y  D  E  V  T  G  V   180


541   CTTAAAGCAGAACCAACAAGTAAAGTAAGCGCTGGTAAAGTTCAAGGTCTAAAATATGGA   600
      ---------+---------+---------+---------+---------+---------+
181   L  K  A  E  P  T  S  K  V  S  A  G  K  V  Q  G  L  K  Y  G   200


601   AATACAGGAGCAACTAACTATACTTCTGGAGCTGAAATATCTGTTCCTACTACAGGCTTA   660
      ---------+---------+---------+---------+---------+---------+
201   N  T  G  A  T  N  Y  T  S  G  A  E  I  S  V  P  T  T  G  L   220
```

Fig. 9B

```
 661  ACATTAACTGCTGATACAACTGCAACAACAGATGTAAATATTTCTGATGTTATGAGTGCA   720
      ---------+---------+---------+---------+---------+---------+
 221   T  L  T  A  D  T  T  A  T  T  D  V  N  I  S  D  V  M  S  A    240


 721  TTTAAATTTAATGGTACTGATACGATTAGTGGATTCCCAGCTGGTTCATCAGCTTCTACT   780
      ---------+---------+---------+---------+---------+---------+
 241   F  K  F  N  G  T  D  T  I  S  G  F  P  A  G  S  S  A  S  T    260


 781  CTTAGAGCAAGTATAAAAGTAATAAATGCAAAAGAAGAATCTATAGATGTTGATTCAAGT   840
      ---------+---------+---------+---------+---------+---------+
 261   L  R  A  S  I  K  V  I  N  A  K  E  E  S  I  D  V  D  S  S    280


 841  TCACATAGAACAGCTGAAGATTTAGCTGAAAAATATGTATTTAAACCAGAAGATGTGAAT   900
      ---------+---------+---------+---------+---------+---------+
 281   S  H  R  T  A  E  D  L  A  E  K  Y  V  F  K  P  E  D  V  N    300


 901  AAAACTTATGAGGCACTGACTGATTTATATAAAGAAGGTATAACAAGTAATCTTATCACT   960
      ---------+---------+---------+---------+---------+---------+
 301   K  T  Y  E  A  L  T  D  L  Y  K  E  G  I  T  S  N  L  I  T    320


 961  CAAGATGGTGGAAAATATCAAGTTGTTTTATTTGCTCAAGGAAAGAGATTAACTACTAAA   1020
      ---------+---------+---------+---------+---------+---------+
 321   Q  D  G  G  K  Y  Q  V  V  L  F  A  Q  G  K  R  L  T  T  K    340


1021  GGAGCAACTGGAACTTTAGCAGATGAAAATTCTCCTCTTAAAGTAACAATAAAAGCAGAT   1080
      ---------+---------+---------+---------+---------+---------+
 341   G  A  T  G  T  L  A  D  E  N  S  P  L  K  V  T  I  K  A  D    360
       ◆

1081  AAAGTAAAAGACTTAAAAGATTATGTTGAAGATTTAAAAAAATGCTAACAATGGATATTCA   1140
      ---------+---------+---------+---------+---------+---------+
 361   K  V  K  D  L  K  D  Y  V  E  D  L  K  N  A  N  N  G  Y  S    380


1141  AATTCTGTTGTTGTAGCAGGTGAAGATAGAATAGAAACAGCAATAGAGTTAAGTAGCAAA   1200
      ---------+---------+---------+---------+---------+---------+
 381   N  S  V  V  V  A  G  E  D  R  I  E  T  A  I  E  L  S  S  K    400


1201  TACTATAACTCTGATGATGACAATGCAATAACTAAAGATCCAGTTAACAATGTTGTTTTA   1260
      ---------+---------+---------+---------+---------+---------+
 401   Y  Y  N  S  D  D  D  N  A  I  T  K  D  P  V  N  N  V  V  L    420


1261  GTTGGTTCTCAAGCTGTAGTTGATGGGCTTGTAGCTTCACCTTTAGCATCTGAAAAAAGA   1320
      ---------+---------+---------+---------+---------+---------+
 421   V  G  S  Q  A  V  V  D  G  L  V  A  S  P  L  A  S  E  K  R    440


1321  GCTCCTTTACTATTAACTTCAGCAGGAAAATTAGATTCAAGTGTTAAAGCTGAGTTGAAA   1380
      ---------+---------+---------+---------+---------+---------+
 441   A  P  L  L  L  T  S  A  G  K  L  D  S  S  V  K  A  E  L  K    460


1381  AGAGTAATGGATTTAAAAATCTACAACAGGTGTAAATACTTCTAAAAAAGTTTACTTAGCT   1440
      ---------+---------+---------+---------+---------+---------+
 461   R  V  M  D  L  K  S  T  T  G  V  N  T  S  K  K  V  Y  L  A    480
```

Fig. 9C

```
1441  GGTGGAGTAAACTCTATATCTAAAGATGTAGAAAATGAATTAAAAGATATGGGACTTAAA  1500
      ---------+---------+---------+---------+---------+---------+
 481  G  G  V  N  S  I  S  K  D  V  E  N  E  L  K  D  M  G  L  K    500


1501  GTTACAAGATTATCAGGAGATGATAGATATGAAACTTCTTTAGCTATAGCTGATGAAATA  1560
      ---------+---------+---------+---------+---------+---------+
 501  V  T  R  L  S  G  D  D  R  Y  E  T  S  L  A  I  A  D  E  I    520


1561  GGTCTTGATAATGATAAAGCTTTTGTAGTTGGAGGAACAGGATTAGCGGATGCTATGAGT  1620
      ---------+---------+---------+---------+---------+---------+
 521  G  L  D  N  D  K  A  F  V  V  G  G  T  G  L  A  D  A  M  S    540


1621  ATAGCTCCAGTTGCTTCTCAATTAAGAAACTCAAATGGAGAACTTGACTTAAAAGGTGAT  1680
      ---------+---------+---------+---------+---------+---------+
 541  I  A  P  V  A  S  Q  L  R  N  S  N  G  E  L  D  L  K  G  D    560


1681  GCAACTCCAATAGTAGTTGTTGATGGAAAAGCTAAAGATATAAATTCTGAAGTAAAAGAT  1740
      ---------+---------+---------+---------+---------+---------+
 561  A  T  P  I  V  V  V  D  G  K  A  K  D  I  N  S  E  V  K  D    580


1741  TTCTTAGATGATTCACAAGTTGATATAATAGGTGGTGTAAATAGTGTTTCTAAAGAAGTA  1800
      ---------+---------+---------+---------+---------+---------+
 581  F  L  D  D  S  Q  V  D  I  I  G  G  V  N  S  V  S  K  E  V    600


1801  ATGGAAGCAATAGATGATGCTACTGGAAAATCACCTGAGAGATATAGTGGAGAAGATAGA  1860
      ---------+---------+---------+---------+---------+---------+
 601  M  E  A  I  D  D  A  T  G  K  S  P  E  R  Y  S  G  E  D  R    620


1861  CAAGCAACAAATGCTAAAGTTATAAAAGAAGATGATTTCTTTAAAAATGGAGAAGTTACA  1920
      ---------+---------+---------+---------+---------+---------+
 621  Q  A  T  N  A  K  V  I  K  E  D  D  F  F  K  N  G  E  V  T    640


1921  AACTTCTTTGTAGCTAAAGATGGTTCAACTAAAGAAGATCAATTAGTAGATGCTTTAGCA  1980
      ---------+---------+---------+---------+---------+---------+
 641  N  F  F  V  A  K  D  G  S  T  K  E  D  Q  L  V  D  A  L  A    660


1981  GGTGCTGCAATTGCTGGTAACTTTGGTGTAACAGTAGATAATGAAGGAAAACCTACAGTT  2040
      ---------+---------+---------+---------+---------+---------+
 661  G  A  A  I  A  G  N  F  G  V  T  V  D  N  E  G  K  P  T  V    680


2041  GCTGATAAAAAAGCTTCTCCAGCACCAATTGTTTTAGCAACAGATTCTTTATCTTCTGAT  2100
      ---------+---------+---------+---------+---------+---------+
 681  A  D  K  K  A  S  P  A  P  I  V  L  A  T  D  S  L  S  S  D    700


2101  CAAAATGTAGCTATAAGTAAAGCTGTAAATGATGACGCTAATACTAAGAATCTAGTTCAA  2160
      ---------+---------+---------+---------+---------+---------+
 701  Q  N  V  A  I  S  K  A  V  N  D  D  A  N  T  K  N  L  V  Q    720
```

Fig. 9D

```
2161  GTTGGTAAAGGTATAGCTACTTCAGTTGTAAGTAAAATAAAAGATTTATTAGATATG  2217
      ---------+---------+---------+---------+---------+-------
 721   V  G  K  G  I  A  T  S  V  V  S  K  I  K  D  L  L  D  M    739
```

Fig. 10A

SEQ ID No 9. Nucleotide sequence of *slpA* from *Clostridium difficile* strain 170444, PCR type 46, with translation. The putative secretory signal cleavage site (Δ) and site of cleavage to form the two mature SLPs (♦) are indicated.

```
  1 ATGAATAAGAAAAATATAGCAATAGCTATGTCAGGTTTAACAGTTTTAGCTTCGGCTGCT  60
    ---------+---------+---------+---------+---------+---------+
  1 M  N  K  K  N  I  A  I  A  M  S  G  L  T  V  L  A  S  A  A   20


 61 CCTGTTTTTGCTGCAACTACTGGAACACAAGGTTATACTGTAGTTAAAAACGACTGGAAA 120
    ---------+---------+---------+---------+---------+---------+
 21 P  V  F  A  A  T  T  G  T  Q  G  Y  T  V  V  K  N  D  W  K   40
                Δ

121 AAAGCAGTAAAACAATTACAAGATGGACTAAAAGATAATAGTATAGGAAAGATAACTGTA 180
    ---------+---------+---------+---------+---------+---------+
 41 K  A  V  K  Q  L  Q  D  G  L  K  D  N  S  I  G  K  I  T  V   60


181 TCTTTTAATGATGGGGTTGTGGGTGAAGTAGCTCCTAAAAGTGCTAATAAGAAAGCGGAC 240
    ---------+---------+---------+---------+---------+---------+
 61 S  F  N  D  G  V  V  G  E  V  A  P  K  S  A  N  K  K  A  D   80


241 AGAGATGCTGCAGCTGAGAAGTTATATAATCTTGTTAACACTCAATTAGATAAATTAGGT 300
    ---------+---------+---------+---------+---------+---------+
 81 R  D  A  A  A  E  K  L  Y  N  L  V  N  T  Q  L  D  K  L  G  100


301 GATGGAGATTATGTTGATTTTTCTGTAGATTATAATTTAGAAAAAAAAATAATAACTAAT 360
    ---------+---------+---------+---------+---------+---------+
101 D  G  D  Y  V  D  F  S  V  D  Y  N  L  E  K  K  I  I  T  N  120


361 CAAGCAGATGCAGAAGCAATTGTTACAAAGTTAAATTCACTTAATGAGAAAACTCTTATT 420
    ---------+---------+---------+---------+---------+---------+
121 Q  A  D  A  E  A  I  V  T  K  L  N  S  L  N  E  K  T  L  I  140


421 GATATAGCAACTAAAGATACTTTTGGAATGGTTAGTAAAACACAAGATAGTGAAGGTAAA 480
    ---------+---------+---------+---------+---------+---------+
141 D  I  A  T  K  D  T  F  G  M  V  S  K  T  Q  D  S  E  G  K  160


481 AATGTTGCTGCAACAAAGGCACTTAAAGTTAAAGATGTTGCTACATTTGGTTTGAAGTCT 540
    ---------+---------+---------+---------+---------+---------+
161 N  V  A  A  T  K  A  L  K  V  K  D  V  A  T  F  G  L  K  S  180


541 GGTGGAAGCGAAGATACTGGATATGTTATTGAAATGAAAGCAGGAGCTGTAGAGGATAAG 600
    ---------+---------+---------+---------+---------+---------+
181 G  G  S  E  D  T  G  Y  V  I  E  M  K  A  G  A  V  E  D  K  200


601 TATGGTAAAGTTGGAGATAGTACGGCAGGTATTGCAATAAATCTTCCTAGTACTGGACTT 660
    ---------+---------+---------+---------+---------+---------+
201 Y  G  K  V  G  D  S  T  A  G  I  A  I  N  L  P  S  T  G  L  220
```

Fig. 10B

```
661  GAATATGCAGGTAAAGGAACAACAATTGATTTTAATAAAACTTTAAAAGTTGATGTAACA  720
     ---------+---------+---------+---------+---------+---------+
221   E   Y   A   G   K   G   T   T   I   D   F   N   K   T   L   K   V   D   V   T   240


721  GGTGGTTCAACACCTAGTGCTGTAGCTGTAAGTGGTTTTGTAACTAAAGATGATACTGAT  780
     ---------+---------+---------+---------+---------+---------+
241   G   G   S   T   P   S   A   V   A   V   S   G   F   V   T   K   D   D   T   D   260


781  TTAGCAAAATCAGGTACTATAAATGTAAGAGTTATAAATGCAAAAGAAGAATCAATTGAT  840
     ---------+---------+---------+---------+---------+---------+
261   L   A   K   S   G   T   I   N   V   R   V   I   N   A   K   E   E   S   I   D   280


841  ATAGATGCAAGCTCATATACATCAGCTGAAAATTTAGCTAAAAGACATGTATTTGATCCA  900
     ---------+---------+---------+---------+---------+---------+
281   I   D   A   S   S   Y   T   S   A   E   N   L   A   K   R   H   V   F   D   P   300


901  GATGAAATTTCTGAAGCATATAAGGCAATAGTAGCATTACAAAATGATGGTATAGAGTCT  960
     ---------+---------+---------+---------+---------+---------+
301   D   E   I   S   E   A   Y   K   A   I   V   A   L   Q   N   D   G   I   E   S   320


961  AATTTAGTTCAGTTAGTTAATGGAAAATATCAAGTGATTTTTTATCCAGAAGGTAAAAGA  1020
     ---------+---------+---------+---------+---------+---------+
321   N   L   V   Q   L   V   N   G   K   Y   Q   V   I   F   Y   P   E   G   K   R   340


1021 TTAGAAACTAAATCAGCAAATGATACAATAGCTAGTCAAGATACACCAGCTAAAGTAGTT  1080
     ---------+---------+---------+---------+---------+---------+
341   L   E   T   K   S   A   N   D   T   I   A   S   Q   D   T   P   A   K   V   V   360
                     ♦


1081 ATAAAAGCTAATAAATTAAAAGATTTAAAAGATTATGTAGATGATTTAAAAACATATAAT  1140
     ---------+---------+---------+---------+---------+---------+
361   I   K   A   N   K   L   K   D   L   K   D   Y   V   D   D   L   K   T   Y   N   380


1141 AATACTTATTCAAATGTTGTAACAGTAGCAGGAGAAGATAGAATAGAAACTGCTATAGAA  1200
     ---------+---------+---------+---------+---------+---------+
381   N   T   Y   S   N   V   V   T   V   A   G   E   D   R   I   E   T   A   I   E   400


1201 TTAAGTAGTAAATATTATAATTCTGATGATAAAAATGCAATAACTGATAAAGCAGTTAAT  1260
     ---------+---------+---------+---------+---------+---------+
401   L   S   S   K   Y   Y   N   S   D   D   K   N   A   I   T   D   K   A   V   N   420


1261 GATATAGTATTAGTTGGATCTACATCTATAGTTGATGGTCTTGTTGCATCACCATTAGCT  1320
     ---------+---------+---------+---------+---------+---------+
421   D   I   V   L   V   G   S   T   S   I   V   D   G   L   V   A   S   P   L   A   440


1321 TCAGAAAAAACAGCTCCATTATTATTAACTTCAAAAGATAAATTAGATTCATCAGTAAAA  1380
     ---------+---------+---------+---------+---------+---------+
441   S   E   K   T   A   P   L   L   L   T   S   K   D   K   L   D   S   S   V   K   460


1381 TCTGAAATAAAGAGAGTTATGAACTTAAAGAGTGACACTGGTATAAATACTTCTAAAAAA  1440
     ---------+---------+---------+---------+---------+---------+
461   S   E   I   K   R   V   M   N   L   K   S   D   T   G   I   N   T   S   K   K   480
```

Fig. 10C

```
1441  GTTTATTTAGCTGGTGGAGTTAATTCTATATCTAAAGATGTAGAAAATGAATTGAAAAAC  1500
      ---------+---------+---------+---------+---------+---------+
 481   V  Y  L  A  G  G  V  N  S  I  S  K  D  V  E  N  E  L  K  N    500


1501  ATGGGTCTTAAAGTTACTAGATTATCAGGAGAAGACAGATACGAAACTTCTTTAGCAATA  1560
      ---------+---------+---------+---------+---------+---------+
 501   M  G  L  K  V  T  R  L  S  G  E  D  R  Y  E  T  S  L  A  I    520


1561  GCTGATGAAATAGGTCTTGATAATGATAAAGCATTTGTAGTTGGTGGTACTGGATTAGCA  1620
      ---------+---------+---------+---------+---------+---------+
 521   A  D  E  I  G  L  D  N  D  K  A  F  V  V  G  G  T  G  L  A    540


1621  GATGCTATGAGTATAGCTCCAGTTGCTTCTCAACTTAAAGATGGAGATGCTACTCCAATA  1680
      ---------+---------+---------+---------+---------+---------+
 541   D  A  M  S  I  A  P  V  A  S  Q  L  K  D  G  D  A  T  P  I    560


1681  GTAGTTGTAGATGGAAAAGCAAAAGAAATAAGTGATGATGCTAAGAGTTTCTTAGGAACT  1740
      ---------+---------+---------+---------+---------+---------+
 561   V  V  V  D  G  K  A  K  E  I  S  D  D  A  K  S  F  L  G  T    580


1741  TCTGATGTTGATATAATAGGTGGAAAAAATAGCGTATCTAAAGAGATTGAAGAGTCAATA  1800
      ---------+---------+---------+---------+---------+---------+
 581   S  D  V  D  I  I  G  G  K  N  S  V  S  K  E  I  E  E  S  I    600


1801  GATAGTGCAACTGGAAAAACTCCAGATAGAATAAGTGGAGATGATAGACAAGCAACTAAT  1860
      ---------+---------+---------+---------+---------+---------+
 601   D  S  A  T  G  K  T  P  D  R  I  S  G  D  D  R  Q  A  T  N    620


1861  GCTGAAGTTTTAAAAGAAGATGATTATTTCACAGATGGTGAAGTTGTGAATTACTTTGTT  1920
      ---------+---------+---------+---------+---------+---------+
 621   A  E  V  L  K  E  D  D  Y  F  T  D  G  E  V  V  N  Y  F  V    640


1921  GCAAAAGATGGTTCTACTAAAGAAGATCAATTAGTAGATGCCTTAGCAGCAGCACCAATA  1980
      ---------+---------+---------+---------+---------+---------+
 641   A  K  D  G  S  T  K  E  D  Q  L  V  D  A  L  A  A  A  P  I    660


1981  GCAGGTAGATTTAAGGAGTCTCCAGCTCCAATCATACTAGCTACTGATACTTTATCTTCT  2040
      ---------+---------+---------+---------+---------+---------+
 661   A  G  R  F  K  E  S  P  A  P  I  I  L  A  T  D  T  L  S  S    680


2041  GACCAAAATGTAGCTGTAAGTAAAGCAGTTCCTAAAGATGGTGGAACTAACTTAGTTCAA  2100
      ---------+---------+---------+---------+---------+---------+
 681   D  Q  N  V  A  V  S  K  A  V  P  K  D  G  G  T  N  L  V  Q    700


2101  GTAGGTAAAGGTATAGCTTCTTCAGTTATAAACAAAATGAAAGATTTATTAGATATG  2157
      ---------+---------+---------+---------+---------+-------
 701   V  G  K  G  I  A  S  S  V  I  N  K  M  K  D  L  L  D  M   719
```

Fig. 11A

SEQ ID No 10. Nucleotide sequence of *slpA* from *Clostridium difficile* strain 170426, PCR type 92, with translation. The putative secretory signal cleavage site (Δ) and site of cleavage to form the two mature SLPs (♦) are indicated.

```
  1   ATGAATAAGAAAAATATAGCAATAGCTATGTCAGGTTTAACAGTTTTAGCTTCGGCTGCT   60
      ---------+---------+---------+---------+---------+---------+
  1   M   N   K   K   N   I   A   I   A   M   S   G   L   T   V   L   A   S   A   A    20


 61   CCTGTTTTTGCTGCAACTACTGGAACACAAGGTTATACTGTAGTTAAAAACGACTGGAAA   120
      ---------+---------+---------+---------+---------+---------+
 21   P   V   F   A   A   T   T   G   T   Q   G   Y   T   V   V   K   N   D   W   K    40
                  Δ

121   AAAGCAGTAAAACAATTACAGGATGGACTAAAAGATAATAGTATAGGAAAGATAACTGTA   180
      ---------+---------+---------+---------+---------+---------+
 41   K   A   V   K   Q   L   Q   D   G   L   K   D   N   S   I   G   K   I   T   V    60


181   TCTTTTAATGATGGGGTTGTGGGTGAAGTAGCTCCTAAAAGTGCTAATAAGAAAGCGGAC   240
      ---------+---------+---------+---------+---------+---------+
 61   S   F   N   D   G   V   V   G   E   V   A   P   K   S   A   N   K   K   A   D    80


241   AGAGATGCTGCAGCTGAGAAGTTATATAATCTTGTTAACACTCAATTAGATAAATTAGGT   300
      ---------+---------+---------+---------+---------+---------+
 81   R   D   A   A   A   E   K   L   Y   N   L   V   N   T   Q   L   D   K   L   G   100


301   GATGGAGATTATGTTGATTTTTCTGTAGATTATAATTTAGAAAAAAAAATAATAACTAAT   360
      ---------+---------+---------+---------+---------+---------+
101   D   G   D   Y   V   D   F   S   V   D   Y   N   L   E   K   K   I   I   T   N   120


361   CAAGCAGATGCAGAAGCAATTGTTACAAAGTTAAATTCACTTAATGAGAAAACTCTTATT   420
      ---------+---------+---------+---------+---------+---------+
121   Q   A   D   A   E   A   I   V   T   K   L   N   S   L   N   E   K   T   L   I   140


421   GATATAGCAACTAAAGATACTTTTGGAATGGTTAGTAAAACACAAGATAGTGAAGGTAAA   480
      ---------+---------+---------+---------+---------+---------+
141   D   I   A   T   K   D   T   F   G   M   V   S   K   T   Q   D   S   E   G   K   160


481   AATGTTGCTGCAACAAAGGCACTTAAAGTTAAAGATGTTGCTACATTTGGTTTGAAGTCT   540
      ---------+---------+---------+---------+---------+---------+
161   N   V   A   A   T   K   A   L   K   V   K   D   V   A   T   F   G   L   K   S   180


541   GGTGGAAGCGAAGATACTGGATATGTTGTTGAAATGAAAGCAGGAGCTGTAGAGGATAAG   600
      ---------+---------+---------+---------+---------+---------+
181   G   G   S   E   D   T   G   Y   V   V   E   M   K   A   G   A   V   E   D   K   200


601   TATGGTAAAGTTGGAGATAGTACGGCAGGTATTGCAATAAATCTTCCTAGTACTGGACTT   660
      ---------+---------+---------+---------+---------+---------+
201   Y   G   K   V   G   D   S   T   A   G   I   A   I   N   L   P   S   T   G   L   220
```

Fig. 11B

```
 661  GAATATGCAGGTAAAGGAACAACAATTGATTTTAATAAAACTTTAAAAGTTGATGTAACA   720
      ---------+---------+---------+---------+---------+---------+
 221  E  Y  A  G  K  G  T  T  I  D  F  N  K  T  L  K  V  D  V  T     240


 721  GGTGGTTCAACACCTAGTGCTGTAGCTGTAAGTGGTTTTGTAACTAAAGATGATACTGAT   780
      ---------+---------+---------+---------+---------+---------+
 241  G  G  S  T  P  S  A  V  A  V  S  G  F  V  T  K  D  D  T  D     260


 781  TTAGCAAAATCAGGTACTATAAATGTAAGAGTTATAAATGCAAAAGAAGAATCAATTGAT   840
      ---------+---------+---------+---------+---------+---------+
 261  L  A  K  S  G  T  I  N  V  R  V  I  N  A  K  E  E  S  I  D     280


 841  ATAGATGCAAGCTCATATACATCAGCTGAAAATTTAGCTAAAAGATATGTATTTGATCCA   900
      ---------+---------+---------+---------+---------+---------+
 281  I  D  A  S  S  Y  T  S  A  E  N  L  A  K  R  Y  V  F  D  P     300


 901  GATGAAATTTCTGAAGCATATAAGGCAATAGTAGCATTACAAAATGATGGTATAGAGTCT   960
      ---------+---------+---------+---------+---------+---------+
 301  D  E  I  S  E  A  Y  K  A  I  V  A  L  Q  N  D  G  I  E  S     320


 961  AATTTAGTTCAGTTAGTTAATGGAAAATATCAAGTGATTTTTTATCCAGAAGGTAAAAGA   1020
      ---------+---------+---------+---------+---------+---------+
 321  N  L  V  Q  L  V  N  G  K  Y  Q  V  I  F  Y  P  E  G  K  R     340


1021  TTAGAAACTAAATCAGCAAATGATACAATAGCTAGTCAAGATACACCAGCTAAAGTAGTT   1080
      ---------+---------+---------+---------+---------+---------+
 341  L  E  T  K  S  A  N  D  T  I  A  S  Q  D  T  P  A  K  V  V     360
                      ◆

1081  ATAAAAGCTAATAAATTAAAAGATTTAAAAGATTATGTAGATGATTTAAAAAACATATAAT   1140
      ---------+---------+---------+---------+---------+---------+
 361  I  K  A  N  K  L  K  D  L  K  D  Y  V  D  D  L  K  T  Y  N     380


1141  AATACTTATTCAAATGTTGTAACAGTAGCAGGAGAAGATAGAATAGAAACTGCTATAGAA   1200
      ---------+---------+---------+---------+---------+---------+
 381  N  T  Y  S  N  V  V  T  V  A  G  E  D  R  I  E  T  A  I  E     400


1201  TTAAGTAGTAAATATTATAATTCTGATGATAAAAATGCAATAACTGATAAAGCAGTTAAT   1260
      ---------+---------+---------+---------+---------+---------+
 401  L  S  S  K  Y  Y  N  S  D  D  K  N  A  I  T  D  K  A  V  N     420


1261  GATATAGTATTAGTTGGATCTACATCTATAGTTGATGGTCTTGTTGCATCACCATTAGCT   1320
      ---------+---------+---------+---------+---------+---------+
 421  D  I  V  L  V  G  S  T  S  I  V  D  G  L  V  A  S  P  L  A     440


1321  TCAGAAAAAACAGCTCCATTATTATTAACTTCAAAAGATAAATTAGATTCATCAGTAAAA   1380
      ---------+---------+---------+---------+---------+---------+
 441  S  E  K  T  A  P  L  L  L  T  S  K  D  K  L  D  S  S  V  K     460


1381  TCTGAAATAAAGAGAGTTATGAACTTAAAGAGTGACACTGGTATAAATACTTCTAAAAAA   1440
      ---------+---------+---------+---------+---------+---------+
 461  S  E  I  K  R  V  M  N  L  K  S  D  T  G  I  N  T  S  K  K     480
```

Fig. 11C

```
1441  GTTTATTTAGCTGGTGGAGTTAATTCTATATCTAAAGATGTAGAAAATGAATTGAAAAAC  1500
      ---------+---------+---------+---------+---------+---------+
 481   V   Y   L   A   G   G   V   N   S   I   S   K   D   V   E   N   E   L   K   N   500


1501  ATGGGTCTTAAAGTTACTAGATTATCAGGAGAAGACAGATACGAAACTTCTTTAGCAATA  1560
      ---------+---------+---------+---------+---------+---------+
 501   M   G   L   K   V   T   R   L   S   G   E   D   R   Y   E   T   S   L   A   I   520


1561  GCTGATGAAATAGGTCTTGATAATGATAAAGCATTTGTAGTTGGTGGTACTGGATTAGCA  1620
      ---------+---------+---------+---------+---------+---------+
 521   A   D   E   I   G   L   D   N   D   K   A   F   V   V   G   G   T   G   L   A   540


1621  GATGCTATGAGTATAGCTCCAGTTGCTTCTCAACTTAAAGATGGAGATGCTACTCCAATA  1680
      ---------+---------+---------+---------+---------+---------+
 541   D   A   M   S   I   A   P   V   A   S   Q   L   K   D   G   D   A   T   P   I   560


1681  GTAGTTGTAGATGGAAAAGCAAAAGAAATAAGTGATGATGCTAAGAGTTTCTTAGGAACT  1740
      ---------+---------+---------+---------+---------+---------+
 561   V   V   V   D   G   K   A   K   E   I   S   D   D   A   K   S   F   L   G   T   580


1741  TCTGATGTTGATATAATAGGTGGAAAAAATAGCGTATCTAAAGAGATTGAAGAGTCAATA  1800
      ---------+---------+---------+---------+---------+---------+
 581   S   D   V   D   I   I   G   G   K   N   S   V   S   K   E   I   E   E   S   I   600


1801  GATAGTGCAACTGGAAAAACTCCAGATAGAATAAGTGGAGATGATAGACAAGCAACTAAT  1860
      ---------+---------+---------+---------+---------+---------+
 601   D   S   A   T   G   K   T   P   D   R   I   S   G   D   D   R   Q   A   T   N   620


1861  GCTGAAGTTTTAAAAGAAGATGATTATTTCACAGATGGTGAAGTTGTGAATTACTTTGTT  1920
      ---------+---------+---------+---------+---------+---------+
 621   A   E   V   L   K   E   D   D   Y   F   T   D   G   E   V   V   N   Y   F   V   640


1921  GCAAAAGATGGTTCTACTAAAGAAGATCAATTAGTAGATGCCTTAGCAGCAGCACCAATA  1980
      ---------+---------+---------+---------+---------+---------+
 641   A   K   D   G   S   T   K   E   D   Q   L   V   D   A   L   A   A   A   P   I   660


1981  GCAGGTAGATTTAAGGAGTCTCCAGCTCCAATCATACTAGCTACTGATACTTTATCTTCT  2040
      ---------+---------+---------+---------+---------+---------+
 661   A   G   R   F   K   E   S   P   A   P   I   I   L   A   T   D   T   L   S   S   680


2041  GACCAAAATGTAGCTGTAAGTAAAGCAGTTCCTAAAGATGGTGGAACTAACTTAGTTCAA  2100
      ---------+---------+---------+---------+---------+---------+
 681   D   Q   N   V   A   V   S   K   A   V   P   K   D   G   G   T   N   L   V   Q   700


2101  GTAGGTAAAGGTATAGCTTCTTCAGTTATAAACAAAATGAAAGATTTATTAGATATG     2157
      ---------+---------+---------+---------+---------+-------
 701   V   G   K   G   I   A   S   S   V   I   N   K   M   K   D   L   L   D   M       719
```